

0420

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ENTERED

## RAW SEQUENCE LISTING

DATE: 07/18/2002

PATENT APPLICATION: US/10/071,894

TIME: 12:44:45

Input Set : A:\0399.2026-001 Sequence Listing.txt

Output Set: N:\CRF3\07182002\J071894.raw

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4 <110> APPLICANT: Lorenz, Michael C.
5   Fink, Gerald R.
7 <120> TITLE OF INVENTION: Glyoxylate Cycle Enzymes as Targets for
8   Antifungal Drug Development
11 <130> FILE REFERENCE: 0399.2026-001
13 <140> CURRENT APPLICATION NUMBER: 10/071,894
14 <141> CURRENT FILING DATE: 2002-02-08
16 <150> PRIOR APPLICATION NUMBER: 60/267,622
17 <151> PRIOR FILING DATE: 2001-02-09
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 550
25 <212> TYPE: PRT
26 <213> ORGANISM: C. albicans ICL1
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31 Lys Glu Val Ala Glu Ile Lys Lys Trp Trp Ser Glu Pro Arg Trp Arg
32 20 25 30
33 Lys Thr Lys Arg Ile Tyr Ser Ala Glu Asp Ile Ala Lys Lys Arg Gly
34 35 40 45
35 Thr Leu Lys Ile Asn His Pro Ser Ser Gln Gln Ala Asp Lys Leu Phe
36 50 55 60
37 Lys Leu Leu Glu Thr His Asp Ala Asp Lys Thr Val Ser Phe Thr Phe
38 65 70 75 80
39 Gly Ala Leu Asp Pro Ile His Val Ala Gln Met Ala Lys Tyr Leu Asp
40 85 90 95
41 Ser Ile Tyr Val Ser Gly Trp Gln Cys Ser Ser Thr Ala Ser Thr Ser
42 100 105 110
43 Asn Glu Pro Ser Pro Asp Leu Ala Asp Tyr Pro Met Asp Thr Val Pro
44 115 120 125
45 Asn Lys Val Glu His Leu Trp Phe Ala Gln Leu Phe His Asp Arg Lys
46 130 135 140
47 Gln Arg Glu Glu Arg Leu Thr Leu Ser Lys Glu Glu Arg Ala Lys Thr
48 145 150 155 160
49 Pro Tyr Ile Asp Phe Leu Arg Pro Ile Ile Ala Asp Ala Asp Thr Gly
50 165 170 175
51 His Gly Gly Ile Thr Ala Ile Ile Lys Leu Thr Lys Met Phe Ile Glu
52 180 185 190
53 Arg Gly Ala Ala Gly Ile His Ile Glu Asp Gln Ala Pro Gly Thr Lys
54 195 200 205
55 Lys Cys Gly His Met Ala Gly Lys Val Leu Val Pro Val Gln Glu His

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56      210      215      220
57 Ile Asn Arg Leu Val Ala Ile Arg Ala Ser Ala Asp Ile Phe Gly Ser
58 225      230      235      240
59 Asn Leu Leu Ala Val Ala Arg Thr Asp Ser Glu Ala Ala Thr Leu Ile
60      245      250      255
61 Thr Ser Thr Ile Asp His Arg Asp His Tyr Phe Ile Ile Gly Ala Thr
62      260      265      270
63 Asn Pro Glu Ala Gly Asp Leu Ala Ala Leu Met Ala Glu Ala Glu Ser
64      275      280      285
65 Lys Gly Ile Tyr Gly Asn Glu Leu Ala Ala Ile Glu Ser Glu Trp Thr
66      290      295      300
67 Lys Lys Ala Gly Leu Lys Leu Phe His Glu Ala Val Ile Asp Glu Ile
68 305      310      315      320
69 Lys Asn Gly Asn Tyr Ser Asn Lys Asp Ala Leu Ile Lys Lys Phe Thr
70      325      330      335
71 Asp Lys Val Asn Pro Leu Ser His Thr Ser His Lys Glu Ala Lys Lys
72      340      345      350
73 Leu Ala Lys Glu Leu Thr Gly Lys Asp Ile Tyr Phe Asn Trp Asp Val
74      355      360      365
75 Ala Arg Ala Arg Glu Gly Tyr Tyr Arg Tyr Gln Gly Gly Thr Gln Cys
76      370      375      380
77 Ala Val Met Arg Gly Arg Ala Phe Ala Pro Tyr Ala Asp Leu Ile Trp
78 385      390      395      400
79 Met Glu Ser Ala Leu Pro Asp Tyr Ala Gln Ala Lys Glu Phe Ala Asp
80      405      410      415
81 Gly Val Lys Ala Ala Val Pro Asp Gln Trp Leu Ala Tyr Asn Leu Ser
82      420      425      430
83 Pro Ser Phe Asn Trp Asn Lys Ala Met Pro Ala Asp Glu Gln Glu Thr
84      435      440      445
85 Tyr Ile Lys Arg Leu Gly Lys Leu Gly Tyr Val Trp Gln Phe Ile Thr
86      450      455      460
87 Leu Ala Gly Leu His Thr Thr Ala Leu Ala Val Asp Asp Phe Ser Asn
88 465      470      475      480
89 Gln Tyr Ser Gln Ile Gly Met Lys Ala Tyr Gly Gln Thr Val Gln Gln
90      485      490      495
91 Pro Glu Ile Glu Lys Gly Val Glu Val Val Lys His Gln Lys Trp Ser
92      500      505      510
93 Gly Ala Thr Tyr Ile Asp Gly Leu Leu Lys Met Val Ser Gly Gly Val
94      515      520      525
95 Thr Ser Thr Ala Ala Met Gly Gln Gly Val Thr Glu Asp Gln Phe Lys
96      530      535      540
97 Glu Ser Lys Ala Lys Ala
98 545      550
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 557
103 <212> TYPE: PRT
104 <213> ORGANISM: S. cerevisiae ICL1
106 <400> SEQUENCE: 2
107 Met Pro Ile Pro Val Gly Asn Thr Lys Asn Asp Phe Ala Ala Leu Gln

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108	1				5				10				15				
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110				20					25				30				
111	Ser	Arg	Trp	Ser	Lys	Thr	Lys	Arg	Asn	Tyr	Ser	Ala	Arg	Asp	Ile	Ala	
112			35					40					45				
113	Val	Arg	Arg	Gly	Thr	Phe	Pro	Pro	Ile	Glu	Tyr	Pro	Ser	Ser	Val	Met	
114		50					55					60					
115	Ala	Arg	Lys	Leu	Phe	Lys	Val	Leu	Glu	Lys	His	His	Asn	Glu	Gly	Thr	
116	65				70					75					80		
117	Val	Ser	Lys	Thr	Phe	Gly	Ala	Leu	Asp	Pro	Val	Gln	Ile	Ser	Gln	Met	
118				85					90						95		
119	Ala	Lys	Tyr	Leu	Asp	Thr	Ile	Tyr	Ile	Ser	Gly	Trp	Gln	Cys	Ser	Ser	
120			100						105					110			
121	Thr	Ala	Ser	Thr	Ser	Asn	Glu	Pro	Gly	Pro	Asp	Leu	Ala	Asp	Tyr	Pro	
122			115					120					125				
123	Met	Asp	Thr	Val	Pro	Asn	Lys	Val	Glu	His	Leu	Phe	Lys	Ala	Gln	Leu	
124		130					135					140					
125	Phe	His	Asp	Arg	Lys	Gln	Leu	Glu	Ala	Arg	Ser	Lys	Ala	Lys	Ser	Gln	
126	145				150					155					160		
127	Glu	Glu	Leu	Asp	Glu	Met	Gly	Ala	Pro	Ile	Asp	Tyr	Leu	Thr	Pro	Ile	
128				165					170						175		
129	Val	Ala	Asp	Ala	Asp	Ala	Gly	His	Gly	Gly	Leu	Thr	Ala	Val	Phe	Lys	
130			180					185						190			
131	Leu	Thr	Lys	Met	Phe	Ile	Glu	Arg	Gly	Ala	Ala	Gly	Ile	His	Met	Glu	
132			195					200					205				
133	Asp	Gln	Thr	Ser	Thr	Asn	Lys	Lys	Cys	Gly	His	Met	Ala	Gly	Arg	Cys	
134		210					215					220					
135	Val	Ile	Pro	Val	Gln	Glu	His	Val	Asn	Arg	Leu	Val	Thr	Ile	Arg	Met	
136	225				230					235					240		
137	Cys	Ala	Asp	Ile	Met	His	Ser	Asp	Leu	Ile	Val	Val	Ala	Arg	Thr	Asp	
138				245					250						255		
139	Ser	Glu	Ala	Ala	Thr	Leu	Ile	Ser	Ser	Thr	Ile	Asp	Thr	Arg	Asp	His	
140			260						265					270			
141	Tyr	Phe	Ile	Val	Gly	Ala	Thr	Asn	Pro	Asn	Ile	Glu	Pro	Phe	Ala	Glu	
142			275					280					285				
143	Val	Leu	Asn	Asp	Ala	Ile	Met	Ser	Gly	Ala	Ser	Gly	Gln	Glu	Leu	Ala	
144		290					295					300					
145	Asp	Ile	Glu	Gln	Lys	Trp	Cys	Arg	Asp	Ala	Gly	Leu	Lys	Leu	Phe	His	
146	305				310					315					320		
147	Glu	Ala	Val	Ile	Asp	Glu	Ile	Glu	Arg	Ser	Ala	Leu	Ser	Asn	Lys	Gln	
148				325					330						335		
149	Glu	Leu	Ile	Lys	Lys	Phe	Thr	Ser	Lys	Val	Gly	Pro	Leu	Thr	Glu	Thr	
150			340						345					350			
151	Ser	His	Arg	Glu	Ala	Lys	Lys	Leu	Ala	Lys	Glu	Ile	Leu	Gly	His	Glu	
152			355					360					365				
153	Ile	Phe	Phe	Asp	Trp	Glu	Leu	Pro	Arg	Val	Arg	Glu	Gly	Leu	Tyr	Arg	
154		370					375					380					
155	Tyr	Arg	Gly	Gly	Thr	Gln	Cys	Ser	Ile	Met	Arg	Ala	Arg	Ala	Phe	Ala	
156	385					390					395					400	

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157 Pro Tyr Ala Asp Leu Val Trp Met Glu Ser Asn Tyr Pro Asp Phe Gln
158                               405                               410                               415
159 Gln Ala Lys Glu Phe Ala Glu Gly Val Lys Glu Lys Phe Pro Asp Gln
160                               420                               425                               430
161 Trp Leu Ala Tyr Asn Leu Ser Pro Ser Phe Asn Trp Pro Lys Ala Met
162                               435                               440                               445
163 Ser Val Asp Glu Gln His Thr Phe Ile Gln Arg Leu Gly Asp Leu Gly
164                               450                               455                               460
165 Tyr Ile Trp Gln Phe Ile Thr Leu Ala Gly Leu His Thr Asn Ala Leu
166 465                               470                               475                               480
167 Ala Val His Asn Phe Ser Arg Asp Phe Ala Lys Asp Gly Met Lys Ala
168                               485                               490                               495
169 Tyr Ala Gln Asn Val Gln Gln Arg Glu Met Asp Asp Gly Val Asp Val
170                               500                               505                               510
171 Leu Lys His Gln Lys Trp Ser Gly Ala Glu Tyr Ile Asp Gly Leu Leu
172                               515                               520                               525
173 Lys Leu Ala Gln Gly Gly Val Ser Ala Thr Ala Ala Met Gly Thr Gly
174                               530                               535                               540
175 Val Thr Glu Asp Gln Phe Lys Glu Asn Gly Val Lys Lys
176 545                               550                               555
179 <210> SEQ ID NO: 3
180 <211> LENGTH: 550
181 <212> TYPE: PRT
182 <213> ORGANISM: C. tropicalis ICL
184 <400> SEQUENCE: 3
185 Met Ala Tyr Thr Lys Ile Asp Ile Asn Gln Glu Glu Ala Asp Phe Gln
186 1                               5                               10                               15
187 Lys Glu Val Ala Glu Ile Lys Lys Trp Trp Ser Glu Pro Arg Trp Arg
188                               20                               25                               30
189 Lys Thr Lys Arg Ile Tyr Ser Ala Glu Asp Ile Ala Lys Lys Arg Gly
190                               35                               40                               45
191 Thr Leu Lys Ile Ala Tyr Pro Ser Ser Gln Gln Ser Asp Lys Leu Phe
192                               50                               55                               60
193 Lys Leu Leu Glu Lys His Asp Ala Glu Lys Ser Val Ser Phe Thr Phe
194 65                               70                               75                               80
195 Gly Ala Leu Asp Pro Ile His Val Ala Gln Met Ala Lys Tyr Leu Asp
196                               85                               90                               95
197 Ser Ile Tyr Val Ser Gly Trp Gln Cys Ser Ser Thr Ala Ser Thr Ser
198                               100                              105                              110
199 Asn Glu Pro Ser Pro Asp Leu Ala Asp Tyr Pro Met Asp Thr Val Pro
200                               115                              120                              125
201 Asn Lys Val Glu His Leu Trp Phe Ala Gln Leu Phe His Asp Arg Lys
202                               130                              135                              140
203 Gln Arg Glu Glu Arg Leu Asn Met Thr Lys Glu Glu Arg Ala Asn Thr
204 145                              150                              155                              160
205 Pro Tyr Ile Asp Phe Leu Arg Pro Ile Ile Ala Asp Ala Asp Thr Gly
206                               165                              170                              175
207 His Gly Gly Ile Thr Ala Ile Ile Lys Leu Thr Lys Leu Phe Ile Glu
208                               180                              185                              190

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209 Arg Gly Ala Ala Gly Ile His Ile Glu Asp Gln Ala Pro Gly Thr Lys
210      195      200      205
211 Lys Cys Gly His Met Ala Gly Lys Val Leu Val Pro Val Gln Glu His
212      210      215      220
213 Ile Asn Arg Leu Val Ala Ile Arg Ala Ser Ala Asp Ile Phe Gly Ser
214 225      230      235      240
215 Asn Leu Leu Ala Val Ala Arg Thr Asp Ser Glu Ala Ala Thr Leu Ile
216      245      250      255
217 Thr Ser Thr Ile Asp His Arg Asp His Tyr Phe Ile Ile Gly Ala Thr
218      260      265      270
219 Asn Pro Glu Ser Gly Asp Leu Ala Ala Leu Met Ala Glu Ala Glu Ala
220      275      280      285
221 Lys Gly Ile Tyr Gly Asp Glu Leu Ala Arg Ile Glu Thr Glu Trp Thr
222      290      295      300
223 Lys Lys Ala Gly Leu Lys Leu Phe His Glu Ala Val Ile Asp Glu Ile
224 305      310      315      320
225 Lys Ala Gly Asn Tyr Ser Asn Lys Glu Ala Leu Ile Lys Lys Phe Thr
226      325      330      335
227 Asp Lys Val Asn Pro Leu Ser His Thr Ser His Lys Glu Ala Lys Lys
228      340      345      350
229 Leu Ala Lys Glu Leu Thr Gly Lys Asp Ile Tyr Phe Asn Trp Asp Val
230      355      360      365
231 Ala Arg Ala Arg Glu Gly Tyr Tyr Arg Tyr Gln Gly Gly Thr Gln Cys
232      370      375      380
233 Ala Val Met Arg Gly Arg Ala Phe Ala Pro Tyr Ala Asp Leu Ile Trp
234 385      390      395      400
235 Met Glu Ser Ala Leu Pro Asp Tyr Asn Gln Ala Lys Glu Phe Ala Asp
236      405      410      415
237 Gly Val Lys Ala Ala Val Pro Asp Gln Trp Leu Ala Tyr Asn Leu Ser
238      420      425      430
239 Pro Ser Phe Asn Trp Asn Lys Ala Met Pro Ala Asp Glu Gln Glu Thr
240      435      440      445
241 Tyr Ile Lys Arg Leu Gly Gln Leu Gly Tyr Val Trp Gln Phe Ile Thr
242      450      455      460
243 Leu Ala Gly Leu His Thr Thr Ala Leu Ala Val Asp Asp Phe Ala Asn
244 465      470      475      480
245 Gln Tyr Ser Gln Ile Gly Met Arg Ala Tyr Gly Gln Thr Val Gln Gln
246      485      490      495
247 Pro Glu Ile Glu Lys Gly Val Glu Val Val Lys His Gln Lys Trp Ser
248      500      505      510
249 Gly Ala Asn Tyr Ile Asp Gly Leu Leu Arg Met Val Ser Gly Gly Val
250      515      520      525
251 Thr Ser Thr Ala Ala Met Gly Ala Gly Val Thr Glu Asp Gln Phe Lys
252      530      535      540
253 Glu Thr Lys Ala Lys Val
254 545      550
257 <210> SEQ ID NO: 4
258 <211> LENGTH: 537
259 <212> TYPE: PRT

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**VERIFICATION SUMMARY**

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Input Set : A:\0399.2026-001 Sequence Listing.txt

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